

# FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

## Genotyping Report

FMDV serotype: O  
Country: Israel  
Year: 2018  
Batch: WRLFMD/2019/00004  
No. of sequences: 70  
Report date: 14th February 2019  
Report generated by: Nick Knowles  
Report checked by: Jemma Wadsworth



Copyright © 2019 The Pirbright Institute, Ash Road, Pirbright, Woking GU24 0NF, United Kingdom.

www: <http://www.wrlfmd.org/>

email: [reporting@pirbright.ac.uk](mailto:reporting@pirbright.ac.uk)

The contents of this report should not be reproduced without permission.

Virus sample name:	ISR/7/2018
Sender reference:	319212 (3)
Location of origin:	Neve Ur
Country of origin:	Israel
Date of collection:	26/04/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	24/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39818, genome 39819, sequence viba_39820, sequencing info 39821	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39832	ISR/10/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39836	ISR/11/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39840	ISR/12/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/8/2018
Sender reference:	319254 (7)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	27/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39822, genome 39823, sequence viba_39824, sequencing info 39825	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39828	ISR/9/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/9/2018
Sender reference:	319254 (8)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	27/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	22/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39826, genome 39827, sequence viba_39828, sequencing info 39829	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39824	ISR/8/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/10/2018
Sender reference:	319212 (4)
Location of origin:	Neve Ur
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	22/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39830, genome 39831, sequence viba_39832, sequencing info 39833	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39820	ISR/7/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39836	ISR/11/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39840	ISR/12/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/11/2018
Sender reference:	319212 (5)
Location of origin:	Neve Ur
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	22/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39834, genome 39835, sequence viba_39836, sequencing info 39837	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39820	ISR/7/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39832	ISR/10/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39840	ISR/12/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/12/2018
Sender reference:	319212 (6)
Location of origin:	Neve Ur
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	22/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39838, genome 39839, sequence viba_39840, sequencing info 39841	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39820	ISR/7/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39832	ISR/10/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39836	ISR/11/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/13/2018
Sender reference:	319263 (9)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	22/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39842, genome 39843, sequence viba_39844, sequencing info 39845	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39860	ISR/20/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/14/2018
Sender reference:	319263 (10)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	22/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39846, genome 39847, sequence viba_39848, sequencing info 39849	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/15/2018
Sender reference:	319265 (11)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	24/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39850, genome 39851, sequence viba_39852, sequencing info 39853	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39860	ISR/20/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/16/2018
Sender reference:	319259 (13)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	28/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	24/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39854, genome 39855, sequence viba_39856, sequencing info 39857	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	94.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.8	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.9	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/20/2018
Sender reference:	319313 (16)
Location of origin:	Nahal Tavor
Country of origin:	Israel
Date of collection:	29/04/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39858, genome 39859, sequence viba_39860, sequencing info 39861	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/25/2018
Sender reference:	319702 (21)
Location of origin:	Ahim Phalah
Country of origin:	Israel
Date of collection:	03/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39862, genome 39863, sequence viba_39864, sequencing info 39865	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39872	ISR/27/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.9	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/26/2018
Sender reference:	319819 (23)
Location of origin:	Hamadia
Country of origin:	Israel
Date of collection:	03/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39866, genome 39867, sequence viba_39868, sequencing info 39869	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39860	ISR/20/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/27/2018
Sender reference:	319702 (22)
Location of origin:	Ahim Phalah
Country of origin:	Israel
Date of collection:	06/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39870, genome 39871, sequence viba_39872, sequencing info 39873	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39864	ISR/25/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.9	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/28/2018
Sender reference:	319819 (24)
Location of origin:	Hamadia
Country of origin:	Israel
Date of collection:	07/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39874, genome 39875, sequence viba_39876, sequencing info 39877	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.9	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.0	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/29/2018
Sender reference:	319935 (25)
Location of origin:	Moledet
Country of origin:	Israel
Date of collection:	07/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39878, genome 39879, sequence viba_39880, sequencing info 39881	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39884	ISR/30/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39892	ISR/32/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39888	ISR/31/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		90.8	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/30/2018
Sender reference:	319935 (27)
Location of origin:	Moledet
Country of origin:	Israel
Date of collection:	07/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39882, genome 39883, sequence viba_39884, sequencing info 39885	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39892	ISR/32/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39880	ISR/29/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39888	ISR/31/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		90.8	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/31/2018
Sender reference:	319935 (26)
Location of origin:	Moledet
Country of origin:	Israel
Date of collection:	10/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39886, genome 39887, sequence viba_39888, sequencing info 39889	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39884	ISR/30/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39892	ISR/32/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39880	ISR/29/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		90.8	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/32/2018
Sender reference:	319935 (28)
Location of origin:	Moledet
Country of origin:	Israel
Date of collection:	10/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39890, genome 39891, sequence viba_39892, sequencing info 39893	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39884	ISR/30/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39880	ISR/29/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39888	ISR/31/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39844	ISR/13/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		90.8	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/33/2018
Sender reference:	320615 (29)
Location of origin:	Kfar Kisch
Country of origin:	Israel
Date of collection:	16/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39894, genome 39895, sequence viba_39896, sequencing info 39897	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39900	ISR/34/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39860	ISR/20/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/34/2018
Sender reference:	320615 (30)
Location of origin:	Kfar Kisch
Country of origin:	Israel
Date of collection:	16/05/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39898, genome 39899, sequence viba_39900, sequencing info 39901	

### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39844	ISR/13/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36404	ISR/2/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36255	Gazit/317556-470/ISR/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36408	ISR/3/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36412	ISR/4/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39868	ISR/26/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39852	ISR/15/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_36400	ISR/1/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39896	ISR/33/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39860	ISR/20/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15

### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	91.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.7	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/35/2018
Sender reference:	324827 (31)
Location of origin:	Baqa-Jatt
Country of origin:	Israel
Date of collection:	10/07/2018
Host species:	sheep
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39902, genome 39903, sequence viba_39904, sequencing info 39905	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39908	ISR/36/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39912	ISR/37/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39920	ISR/39/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39928	ISR/41/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/36/2018
Sender reference:	324827 (32)
Location of origin:	Baqa-Jatt
Country of origin:	Israel
Date of collection:	10/07/2018
Host species:	sheep
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	23/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39906, genome 39907, sequence viba_39908, sequencing info 39909	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39916	ISR/38/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39912	ISR/37/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39920	ISR/39/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39904	ISR/35/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39928	ISR/41/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/37/2018
Sender reference:	324827 (33)
Location of origin:	Baqa-Jatt
Country of origin:	Israel
Date of collection:	10/07/2018
Host species:	sheep
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39910, genome 39911, sequence viba_39912, sequencing info 39913	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39908	ISR/36/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39920	ISR/39/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39904	ISR/35/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39928	ISR/41/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/38/2018
Sender reference:	324827 (34)
Location of origin:	Baqa-Jatt
Country of origin:	Israel
Date of collection:	12/07/2018
Host species:	sheep
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39914, genome 39915, sequence viba_39916, sequencing info 39917	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39908	ISR/36/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39912	ISR/37/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39920	ISR/39/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39904	ISR/35/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39928	ISR/41/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/39/2018
Sender reference:	324827 (35)
Location of origin:	Baqa-Jatt
Country of origin:	Israel
Date of collection:	12/07/2018
Host species:	sheep
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39918, genome 39919, sequence viba_39920, sequencing info 39921	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39908	ISR/36/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39912	ISR/37/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39904	ISR/35/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39928	ISR/41/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/40/2018
Sender reference:	324827 (36)
Location of origin:	Baqa-Jatt
Country of origin:	Israel
Date of collection:	12/07/2018
Host species:	sheep
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39922, genome 39923, sequence viba_39924, sequencing info 39925	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39908	ISR/36/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39912	ISR/37/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39920	ISR/39/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39904	ISR/35/2018	sheep	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39928	ISR/41/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.5	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.2	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.7	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.4	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/41/2018
Sender reference:	329773 (37)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	08/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39926, genome 39927, sequence viba_39928, sequencing info 39929	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/42/2018
Sender reference:	329773 (39)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	08/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39930, genome 39931, sequence viba_39932, sequencing info 39933	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/43/2018
Sender reference:	329773 (41)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	08/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39934, genome 39935, sequence viba_39936, sequencing info 39937	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/44/2018
Sender reference:	329773 (43)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	08/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39938, genome 39939, sequence viba_39940, sequencing info 39941	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/45/2018
Sender reference:	329773 (38)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	13/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39942, genome 39943, sequence viba_39944, sequencing info 39945	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/46/2018
Sender reference:	329773 (40)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	13/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019

VIBASys IDs: sample 39946, genome 39947, sequence viba\_39948, sequencing info 39949

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/47/2018
Sender reference:	329773 (42)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	13/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019
VIBASys IDs: sample 39950, genome 39951, sequence viba_39952, sequencing info 39953	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39956	ISR/48/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/48/2018
Sender reference:	329773 (44)
Location of origin:	Mughar
Country of origin:	Israel
Date of collection:	13/09/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	13/02/2019
Last updated:	13/02/2019

VIBASys IDs: sample 39954, genome 39955, sequence viba\_39956, sequencing info 39957

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39928	ISR/41/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39952	ISR/47/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39936	ISR/43/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39944	ISR/45/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39932	ISR/42/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39940	ISR/44/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39948	ISR/46/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39908	ISR/36/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39916	ISR/38/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39924	ISR/40/2018	sheep	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	97.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	93.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	92.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	92.3	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		91.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		91.3	0	O	ME-SA	PanAsia-2	TER-08
viba_850	NEP/1/2015	cattle	90.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	90.5	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		90.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/51/2018
Sender reference:	334997 (48)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	02/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39958, genome 39959, sequence viba_39960, sequencing info 39961	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/52/2018
Sender reference:	334997 (49)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	02/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39962, genome 39963, sequence viba_39964, sequencing info 39965	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/53/2018
Sender reference:	334997 (50)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	02/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39966, genome 39967, sequence viba_39968, sequencing info 39969	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/54/2018
Sender reference:	334997 (51)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	02/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39970, genome 39971, sequence viba_39972, sequencing info 39973	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/55/2018
Sender reference:	334997 (52)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	21/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 39974, genome 39975, sequence viba\_39976, sequencing info 39977

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/57/2018
Sender reference:	334997 (54)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	21/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	27/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39978, genome 39979, sequence viba_39980, sequencing info 39981	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/58/2018
Sender reference:	334997 (55)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	21/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39982, genome 39983, sequence viba_39984, sequencing info 39985	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/59/2018
Sender reference:	335278 (56)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	23/11/2018
Host species:	wild boar
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	27/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39986, genome 39987, sequence viba_39988, sequencing info 39989	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40004	ISR/64/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40008	ISR/66/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39996	ISR/62/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39992	ISR/60/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/60/2018
Sender reference:	335278 (57)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	23/11/2018
Host species:	wild boar
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39990, genome 39991, sequence viba_39992, sequencing info 39993	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40004	ISR/64/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39988	ISR/59/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40008	ISR/66/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39996	ISR/62/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/62/2018
Sender reference:	335278 (59)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	23/11/2018
Host species:	wild boar
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39994, genome 39995, sequence viba_39996, sequencing info 39997	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40004	ISR/64/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39988	ISR/59/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40008	ISR/66/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39992	ISR/60/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/63/2018
Sender reference:	335278 (60)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	26/11/2018
Host species:	wild boar
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 39998, genome 39999, sequence viba_40000, sequencing info 40001	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40004	ISR/64/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39988	ISR/59/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40008	ISR/66/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39996	ISR/62/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39992	ISR/60/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/64/2018
Sender reference:	335278 (61)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	26/11/2018
Host species:	wild boar
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40002, genome 40003, sequence viba_40004, sequencing info 40005	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40000	ISR/63/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39988	ISR/59/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40008	ISR/66/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39996	ISR/62/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39992	ISR/60/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/66/2018
Sender reference:	335278 (63)
Location of origin:	Mas ade
Country of origin:	Israel
Date of collection:	27/11/2018
Host species:	wild boar
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40006, genome 40007, sequence viba_40008, sequencing info 40009	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40004	ISR/64/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39988	ISR/59/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39996	ISR/62/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39992	ISR/60/2018	wild boar	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/67/2018
Sender reference:	335670 (64)
Location of origin:	Kefar Sold
Country of origin:	Israel
Date of collection:	29/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40010, genome 40011, sequence viba_40012, sequencing info 40013	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40032	ISR/72/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40028	ISR/71/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40016	ISR/68/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40024	ISR/70/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40020	ISR/69/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.1	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/68/2018
Sender reference:	335670 (65)
Location of origin:	Kefar Sold
Country of origin:	Israel
Date of collection:	29/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40014, genome 40015, sequence viba\_40016, sequencing info 40017

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40032	ISR/72/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40028	ISR/71/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40024	ISR/70/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40012	ISR/67/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40020	ISR/69/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.1	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/69/2018
Sender reference:	335670 (66)
Location of origin:	Kefar Sold
Country of origin:	Israel
Date of collection:	29/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40018, genome 40019, sequence viba_40020, sequencing info 40021	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40032	ISR/72/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40028	ISR/71/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40016	ISR/68/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40024	ISR/70/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40012	ISR/67/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.5	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	95.9	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.7	0	O	ME-SA	PanAsia-2	
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_719	IRN/88/2009		90.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		89.7	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	88.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.8	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.3	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/70/2018
Sender reference:	335670 (67)
Location of origin:	Kefar Sold
Country of origin:	Israel
Date of collection:	30/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	29/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40022, genome 40023, sequence viba\_40024, sequencing info 40025

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40032	ISR/72/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40028	ISR/71/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40016	ISR/68/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40012	ISR/67/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40020	ISR/69/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.1	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/71/2018
Sender reference:	335670 (68)
Location of origin:	Kefar Sold
Country of origin:	Israel
Date of collection:	30/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	30/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40026, genome 40027, sequence viba_40028, sequencing info 40029	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40032	ISR/72/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40016	ISR/68/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40024	ISR/70/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40012	ISR/67/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40020	ISR/69/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.1	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/72/2018
Sender reference:	335670 (69)
Location of origin:	Kefar Sold
Country of origin:	Israel
Date of collection:	30/11/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	30/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40030, genome 40031, sequence viba_40032, sequencing info 40033	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40028	ISR/71/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40016	ISR/68/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40024	ISR/70/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40012	ISR/67/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40020	ISR/69/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.7	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.1	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_719	IRN/88/2009		90.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/73/2018
Sender reference:	335935 (70)
Location of origin:	Kibbutz Snir
Country of origin:	Israel
Date of collection:	03/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	30/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40034, genome 40035, sequence viba_40036, sequencing info 40037	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40044	ISR/75/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40052	ISR/77/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40040	ISR/74/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40048	ISR/76/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40056	ISR/78/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40080	ISR/84/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	91.5	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.1	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/74/2018
Sender reference:	335935 (71)
Location of origin:	Kibbutz Snir
Country of origin:	Israel
Date of collection:	03/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40038, genome 40039, sequence viba_40040, sequencing info 40041	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40044	ISR/75/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40052	ISR/77/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40048	ISR/76/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40036	ISR/73/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40056	ISR/78/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40080	ISR/84/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	91.5	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.1	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/75/2018
Sender reference:	335935 (72)
Location of origin:	Kibbutz Snir
Country of origin:	Israel
Date of collection:	03/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	01/02/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40042, genome 40043, sequence viba\_40044, sequencing info 40045

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40052	ISR/77/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40040	ISR/74/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40048	ISR/76/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40036	ISR/73/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40056	ISR/78/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40080	ISR/84/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	91.5	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.1	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/76/2018
Sender reference:	335935 (73)
Location of origin:	Kibbutz Snir
Country of origin:	Israel
Date of collection:	05/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	30/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40046, genome 40047, sequence viba\_40048, sequencing info 40049

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40044	ISR/75/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40052	ISR/77/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40040	ISR/74/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40036	ISR/73/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40056	ISR/78/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40080	ISR/84/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	91.5	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.1	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/77/2018
Sender reference:	335935 (74)
Location of origin:	Kibbutz Snir
Country of origin:	Israel
Date of collection:	05/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	30/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40050, genome 40051, sequence viba\_40052, sequencing info 40053

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40044	ISR/75/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40040	ISR/74/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40048	ISR/76/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40036	ISR/73/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40056	ISR/78/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40080	ISR/84/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	91.5	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.1	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/78/2018
Sender reference:	335935 (75)
Location of origin:	Kibbutz Snir
Country of origin:	Israel
Date of collection:	05/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	30/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40054, genome 40055, sequence viba\_40056, sequencing info 40057

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40044	ISR/75/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40052	ISR/77/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40040	ISR/74/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40048	ISR/76/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40036	ISR/73/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40080	ISR/84/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	99.4	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	91.5	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	89.1	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/79/2018
Sender reference:	336735 (76)
Location of origin:	Lehavot Habashan
Country of origin:	Israel
Date of collection:	12/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	01/02/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40058, genome 40059, sequence viba_40060, sequencing info 40061	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40068	ISR/81/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/80/2018
Sender reference:	336681 (78)
Location of origin:	around Snir
Country of origin:	Israel
Date of collection:	12/12/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40062, genome 40063, sequence viba_40064, sequencing info 40065	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/81/2018
Sender reference:	336735 (77)
Location of origin:	Lehavot Habashan
Country of origin:	Israel
Date of collection:	15/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40066, genome 40067, sequence viba\_40068, sequencing info 40069

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40060	ISR/79/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40072	ISR/82/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.2	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		88.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	



Virus sample name:	ISR/82/2018
Sender reference:	336681 (79)
Location of origin:	around Snir
Country of origin:	Israel
Date of collection:	15/12/2018
Host species:	gazelle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40070, genome 40071, sequence viba_40072, sequencing info 40073	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_39964	ISR/52/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39980	ISR/57/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39976	ISR/55/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39960	ISR/51/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40004	ISR/64/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40000	ISR/63/2018	wild boar	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.7	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.0	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.0	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.1	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.6	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/83/2018
Sender reference:	337513 (80)
Location of origin:	Kibbutz Ortal
Country of origin:	Israel
Date of collection:	24/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40074, genome 40075, sequence viba\_40076, sequencing info 40077

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40080	ISR/84/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40088	ISR/86/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.2	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.8	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/84/2018
Sender reference:	337513 (81)
Location of origin:	Kibbutz Ortal
Country of origin:	Israel
Date of collection:	24/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40078, genome 40079, sequence viba_40080, sequencing info 40081	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40096	ISR/88/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40088	ISR/86/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.2	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.8	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/85/2018
Sender reference:	337513 (82)
Location of origin:	Kibbutz Ortal
Country of origin:	Israel
Date of collection:	24/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40082, genome 40083, sequence viba\_40084, sequencing info 40085

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40080	ISR/84/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40088	ISR/86/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.2	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.8	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/86/2018
Sender reference:	337513 (83)
Location of origin:	Kibbutz Ortal
Country of origin:	Israel
Date of collection:	25/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40086, genome 40087, sequence viba_40088, sequencing info 40089	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40080	ISR/84/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.2	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.8	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/87/2018
Sender reference:	337513 (84)
Location of origin:	Kibbutz Ortal
Country of origin:	Israel
Date of collection:	25/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019

VIBASys IDs: sample 40090, genome 40091, sequence viba\_40092, sequencing info 40093

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40080	ISR/84/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40096	ISR/88/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40088	ISR/86/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.2	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.8	0	O	ME-SA	PanAsia	

Virus sample name:	ISR/88/2018
Sender reference:	337513 (85)
Location of origin:	Kibbutz Ortal
Country of origin:	Israel
Date of collection:	25/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia-2
Sublineage:	QOM-15
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	31/01/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	07/02/2019
Created:	14/02/2019
Last updated:	14/02/2019
VIBASys IDs: sample 40094, genome 40095, sequence viba_40096, sequencing info 40097	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40080	ISR/84/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40092	ISR/87/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40076	ISR/83/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40084	ISR/85/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_40088	ISR/86/2018	cattle	100.0	0	O	ME-SA	PanAsia-2	QOM-15
viba_39964	ISR/52/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39972	ISR/54/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39984	ISR/58/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_40064	ISR/80/2018	gazelle	99.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_39968	ISR/53/2018	cattle	99.8	0	O	ME-SA	PanAsia-2	QOM-15

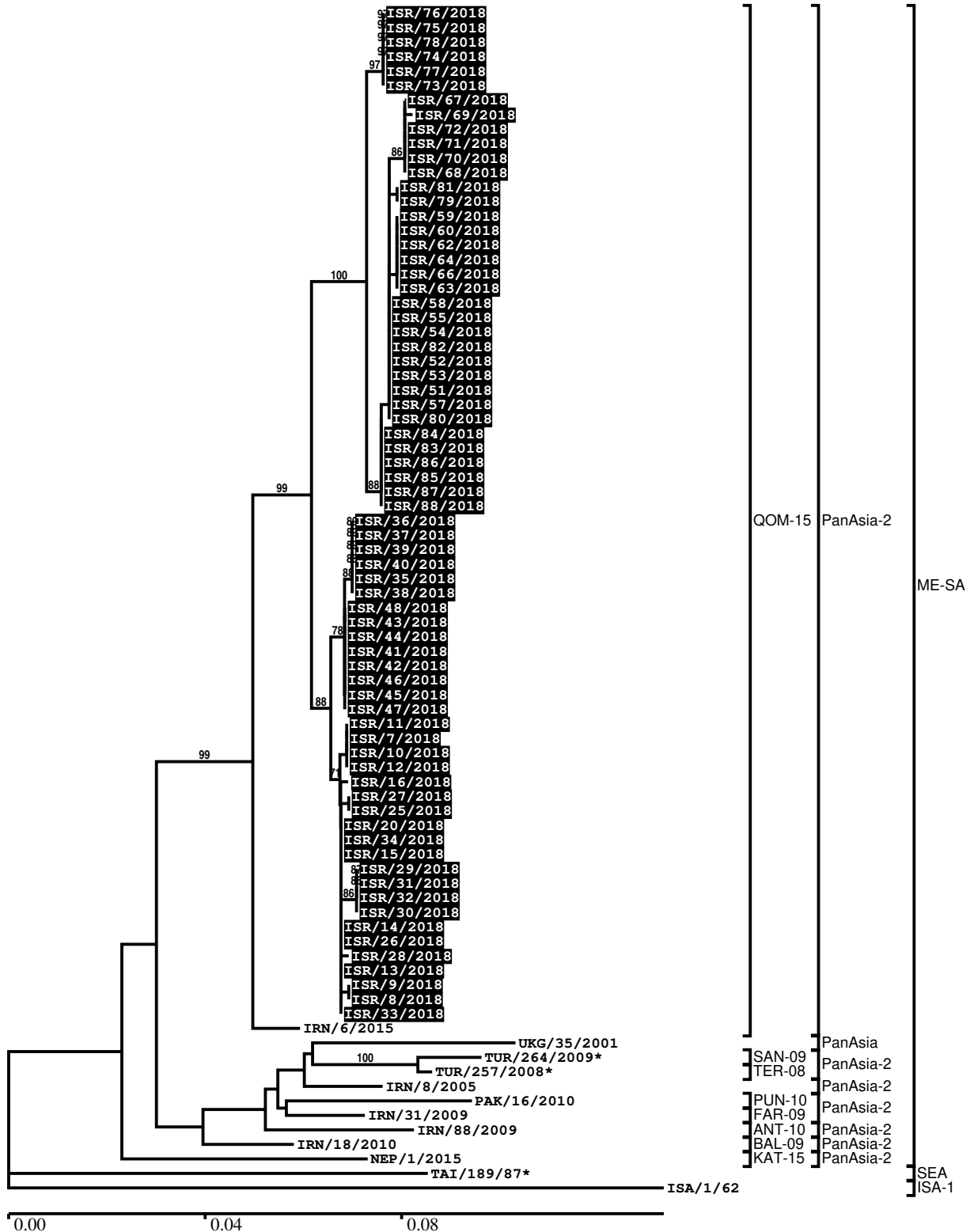
#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_860	IRN/6/2015	cattle	96.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	92.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	91.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	91.2	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		90.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	90.4	1	O	ME-SA	PanAsia-2	KAT-15
viba_491	TUR/257/2008		90.2	0	O	ME-SA	PanAsia-2	TER-08
viba_354	PAK/16/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_505	TUR/264/2009		89.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_285	UKG/35/2001	porcine	88.8	0	O	ME-SA	PanAsia	

Report on FMDV O in Israel in 2018

Batch: WRLFMD/2019/00004



\*, not a WRLFMD Reference Number



## Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2019/00004-Israel-O (70 sequences)
Sequence database set:	allseqs_O (4281 sequences)
Prototype sequence set:	!prototypes_O (49 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	636
Phylogeny reconstruction method:	fdnadist, fneighbor
Number of bootstrap samples:	1000
Random seed for bootstrapping:	1
Displaying bootstrap values above:	70.0%
Number of sequences in tree capped at:	100
Number of prototype sequences in tree:	10
VIBASys version:	reflabs-1.1.2

## Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/O

label	accession	host(s)	lab	country	taxonomic information
ISR/76/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/75/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/78/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/74/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/77/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/73/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/67/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/69/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/72/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/71/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/70/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/68/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/81/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/79/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/59/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/60/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/62/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/64/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/66/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/63/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/58/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/55/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/54/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/82/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/52/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/53/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/51/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/57/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/80/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/84/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/83/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/86/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/85/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/87/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/88/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/36/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15

*continued on next page*

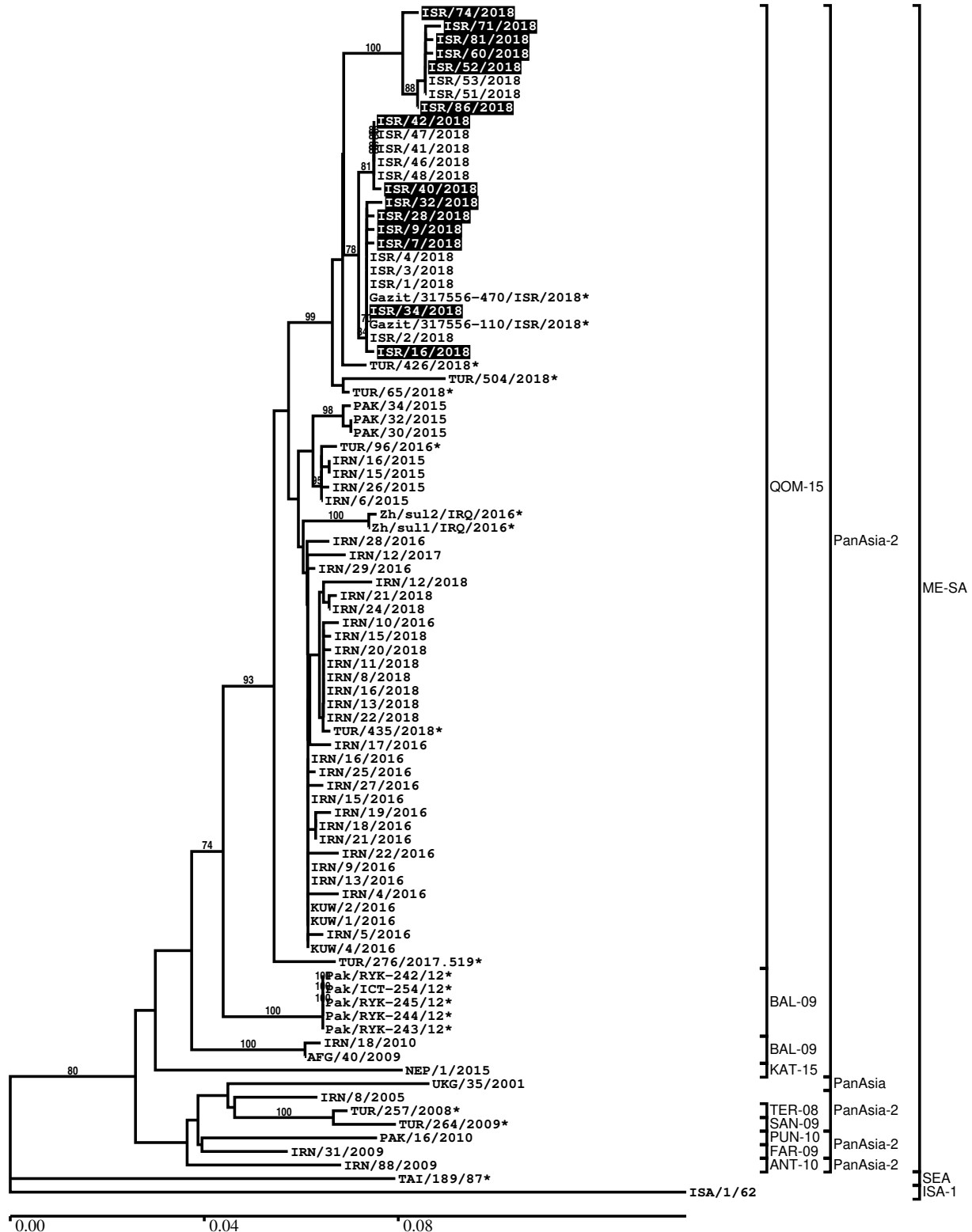
label	accession	host(s)	lab	country	taxonomic information
ISR/37/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/39/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/40/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/35/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/38/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/48/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/43/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/44/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/41/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/42/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/46/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/45/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/47/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/11/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/7/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/10/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/12/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/16/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/27/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/25/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/20/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/34/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/15/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/29/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/31/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/32/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/30/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/14/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/26/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/28/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/13/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/9/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/8/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/33/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
IRN/6/2015	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
TUR/264/2009*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/SAN-09
TUR/257/2008*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/TER-08
IRN/8/2005	KY091281	ovine	WRLFMD	Iran	ME-SA/PanAsia-2
PAK/16/2010	KY091285	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/PUN-10
IRN/31/2009	KY091284	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/FAR-09
IRN/88/2009	KY091282	n/a	WRLFMD	Iran	ME-SA/PanAsia-2/ANT-10
IRN/18/2010	KY091283	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/BAL-09
NEP/1/2015	n/a	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

\*, not a WRLFMD Reference Number

n/a, not available

Report on FMDV O in Israel in 2018

Batch: WRLFMD/2019/00004a-Israel-O



\*, not a WRLFMD Reference Number

## Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2019/00004a-Israel-O-Israel-O (14 sequences)
Sequence database set:	allseqs_O (4225 sequences)
Prototype sequence set:	!prototypes_O (49 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	636
Phylogeny reconstruction method:	fdnadist, fneighbor
Number of bootstrap samples:	1000
Random seed for bootstrapping:	1
Displaying bootstrap values above:	70.0%
Number of sequences in tree capped at:	100
Number of prototype sequences in tree:	10
VIBASys version:	reflabs-1.1.2

## Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/O

label	accession	host(s)	lab	country	taxonomic information
ISR/74/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/71/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/81/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/60/2018	n/a	wild boar	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/52/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/53/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/51/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/86/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/42/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/47/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/41/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/46/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/48/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/40/2018	n/a	sheep	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/32/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/28/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/9/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/7/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/4/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/3/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/1/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
Gazit/317556-470/ISR/2018*	n/a	cattle	KVI	Israel	ME-SA/PanAsia-2/QOM-15
ISR/34/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
Gazit/317556-110/ISR/2018*	n/a	cattle	KVI	Israel	ME-SA/PanAsia-2/QOM-15
ISR/2/2018	n/a	cattle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
ISR/16/2018	n/a	gazelle	WRLFMD	Israel	ME-SA/PanAsia-2/QOM-15
TUR/426/2018*	n/a	n/a	FMDI	Turkey	ME-SA/PanAsia-2/QOM-15
TUR/504/2018*	n/a	n/a	FMDI	Turkey	ME-SA/PanAsia-2/QOM-15
TUR/65/2018*	n/a	n/a	FMDI	Turkey	ME-SA/PanAsia-2/QOM-15
PAK/34/2015	n/a	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/QOM-15
PAK/32/2015	n/a	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/QOM-15
PAK/30/2015	n/a	water buffalo	WRLFMD	Pakistan	ME-SA/PanAsia-2/QOM-15
TUR/96/2016*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/QOM-15
IRN/16/2015	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/15/2015	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/26/2015	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15

*continued on next page*

label	accession	host(s)	lab	country	taxonomic information
IRN/6/2015	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
Zh/sul2/IRQ/2016*	KY412560	n/a	Veterinary Directorate of Sulaimani	Iraq	ME-SA/PanAsia-2/QOM-15
Zh/sul1/IRQ/2016*	KY412559	n/a	Veterinary Directorate of Sulaimani	Iraq	ME-SA/PanAsia-2/QOM-15
IRN/28/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/12/2017	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/29/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/12/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/21/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/24/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/10/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/15/2018	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/20/2018	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/11/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/8/2018	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/16/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/13/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/22/2018	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
TUR/435/2018*	n/a	n/a	FMDI	Turkey	ME-SA/PanAsia-2/QOM-15
IRN/17/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/16/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/25/2016	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/27/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/15/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/19/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/18/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/21/2016	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/22/2016	n/a	sheep	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/9/2016	n/a	dog	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/13/2016	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/4/2016	n/a	n/a	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
KUW/2/2016	n/a	cattle	WRLFMD	Kuwait	ME-SA/PanAsia-2/QOM-15
KUW/1/2016	n/a	cattle	WRLFMD	Kuwait	ME-SA/PanAsia-2/QOM-15
IRN/5/2016	n/a	n/a	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
KUW/4/2016	n/a	cattle	WRLFMD	Kuwait	ME-SA/PanAsia-2/QOM-15
TUR/276/2017.519*	n/a	n/a	FMDI	Turkey	ME-SA/PanAsia-2/QOM-15
Pak/RYK-242/12*	KU365843	cattle	PIADC	Pakistan	ME-SA/PanAsia-2/BAL-09
Pak/ICT-254/12*	KU365828	water buffalo	PIADC	Pakistan	ME-SA/PanAsia-2/BAL-09
Pak/RYK-245/12*	KU365839	cattle	PIADC	Pakistan	ME-SA/PanAsia-2/BAL-09
Pak/RYK-244/12*	KU365838	cattle	PIADC	Pakistan	ME-SA/PanAsia-2/BAL-09
Pak/RYK-243/12*	KU365837	cattle	PIADC	Pakistan	ME-SA/PanAsia-2/BAL-09
IRN/18/2010	KY091283	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/BAL-09
AFG/40/2009	n/a	n/a	WRLFMD	Afghanistan	ME-SA/PanAsia-2/BAL-09
NEP/1/2015	n/a	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
IRN/8/2005	KY091281	ovine	WRLFMD	Iran	ME-SA/PanAsia-2
TUR/257/2008*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/TER-08
TUR/264/2009*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/SAN-09
PAK/16/2010	KY091285	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/PUN-10
IRN/31/2009	KY091284	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/FAR-09
IRN/88/2009	KY091282	n/a	WRLFMD	Iran	ME-SA/PanAsia-2/ANT-10
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

\*, not a WRLFMD Reference Number

n/a, not available